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- (b) identifying the number of single-nucleotide polymorphisms of said plurality in at least weak linkage disequilibrium with each other on said chromosomal regions;
  - (c) comparing the number of single-nucleotide polymorphisms in linkage disequilibrium to the number of haplotypes in said chromosomal regions; and
  - (d) selecting a correlation test, wherein a single nucleotide-based correlation test is selected if the number of single-nucleotide polymorphisms in linkage disequilibrium is smaller than the number of haplotypes, thereby identifying a genetic region associated with responsiveness to an agent.

- 26. The method of claim 25, wherein the haplotype-based correlation test is a regression test.
- 27. The method of claim 25, wherein the haplotype-based correlation test is ANOVA test.

**METHOD OF IDENTIFYING GENETIC REGIONS ASSOCIATED  
WITH DISEASE AND PREDICTING RESPONSIVENESS TO  
THERAPEUTIC AGENTS**

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**ABSTRACT**

The invention relates to a method of identifying genetic regions related to disease and to predicting the response to therapeutic agents. The invention provides a method of identifying a genetic region associated with a disease and/or associated with responsiveness to a therapeutic agent.

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